Package 'RnBeads.mm10'

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Title RnBeads.mm10

Description Automatically generated RnBeads annotation package for the assembly mm10.

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License GPL-3

Version 2.20.0

Depends R (>= 3.5.0), GenomicRanges

Suggests RnBeads

git_url https://git.bioconductor.org/packages/RnBeads.mm10

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`mm10` *Annotation tables for mm10*

Description

Scaffold of annotation tables for the mm10 assembly. This structure is automatically loaded upon initialization of the annotation, that is, by the first valid call to any of the following functions: `rnb.get.assemblies`, `rnb.get.chromosomes`, `rnb.get.annotation`, `rnb.set.annotation`, `rnb.get.mapping`, `rnb.annotation.size`. Adding an annotation amounts to attaching its table(s) and mapping structures to this scaffold.

Format

list of up to six elements - "GENOME", "CHROMOSOMES", "regions", "sites", "controls" and "mappings". These elements are described below.

"GENOME" Name of the Bioconductor package that contains the genomic sequence for this genome assembly.

"CHROMOSOMES" Supported chromosomes for this genome assembly. The elements of this character vector follow the Ensembl convention ("1", "2", ...), and the names of this vector - the convention of the UCSC Genome Browser ("chr1", "chr2", ...).

"regions" list of NULLs; the names of the elements correspond to the built-in region annotation tables. Once the default annotations are loaded, the attribute "builtin" is a logical vector storing, for each region annotation, whether it is the default (built-in) or custom.

"sites" list of NULLs; the names of the elements correspond to the site and probe annotation tables.

"controls" list of NULLs; the names of the elements correspond to the control probe annotation tables. The attribute "sites" is a character vector pointing to the site annotation that encompasses the respective control probes.

"mappings" list of NULLs; the names of the elements correspond to the built-in region annotation tables.

Author(s)

RnBeads Annotation Creator

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rnb.set.annotation, *1*

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